MLVA provided a characteristic strain clustering according to resistance patterns but PFGE failed to do so. The invasive and non-invasive strains were not distinguished by both methods.

Conclusion: The occurrence of high percentage of MDR *S. enteritidis* strains is of public health concern. However, the ability of MLVA to rapidly subtype *S. enteritidis* strains into groups with characteristic antimicrobial resistance patterns may be of great advantage in clinical diagnostic.

http://dx.doi.org/10.1016/j.ijid.2012.05.849

Type: Poster Presentation

Final Abstract Number: 45.059
Session: Bacterial Infections
Date: Friday, June 15, 2012
Time: 12:45-14:15
Room: Poster & Exhibition Area

Molecular and genomic investigations into spreading and diversification of *Vibrio cholerae* O1 in Thailand

K. Okada [1,*], A. Roobthaisong [1], S. Hamada [1], S. Chantaroj [2]

[1] *Thailand-Japan Research Collaboration Center on Emerging and Reemerging Infections, Nonthaburi, Thailand*
[2] *National Institute of Health, Nonthaburi, Thailand*

Background: Cholera epidemics break out occasionally in Thailand. This study aims to characterize *V. cholerae* O1 isolated in Thailand during 2007 to 2010.

Methods: *V. cholerae* O1 isolates collected from cholera patients, their family members, and neighbors, as well as environmental samples in cholera outbreak sites. PCR was carried out for detection of theseveral markers, *rtxC, rstR, ctxA, zot, ace, tcpA, ompU, toxR* and *ctxB* genes. The presence or absence of ORFs in the *Vibrio* seventh pandemic island I (VSP-I) and II (VSP-II) clusters of selected isolates was examined. In addition, the isolates were characterized using pulsed-field gel electrophoresis (PFGE), ribotyping, multilocus variable-number tandem repeat analysis (MLVA).

Results: We found almost all of the 343 isolates obtained carried the classical cholera toxin gene and El Tor *rstR* genes. PFGE differentiated the isolates into 10 distinct pulsotypes, clustered into two major groups. Ribotyping, MLVA, and PCR to detect VSP-II related genes of randomly selected isolates from each pulsotype corresponded to the results obtained by PFGE. MLVA typing among isolates revealed geographical and temporal associations of causative *V. cholerae* in cholera outbreaks. The 2007 cholera outbreaks in northeastern Thailand were triggered by the consumption of cockles contaminated with *V. cholerae* O1 MLVA type 2. On the other hand, outbreaks in the southern Gulf areas outbreaks in 2009 were linked mainly with MLVA types 7 and 12, while those in the central Gulf areas during 2009–2010 were linked with MLVA type 4. MLVA type 41 continued to exist predominantly in an outbreak site for more than three years. Long-term survival of *V. cholerae* O1 of a particular MVLA type, such as type 41, may be attained in watery environments or in humans. It should be noted here that one *V. cholerae* O1 carrying the El Tor type *ctxB* which did belong to neither groups.

pearance of particular type(s) of isolates with special reference to spatial and temporal associations of the organisms.

http://dx.doi.org/10.1016/j.ijid.2012.05.850

Type: Poster Presentation

Final Abstract Number: 45.060
Session: Bacterial Infections
Date: Friday, June 15, 2012
Time: 12:45-14:15
Room: Poster & Exhibition Area

Sepsis due to *Vibrio alginolyticus* isolated from catheter of young patient with hypercholesterolemi: the first case from Turkey

L. Oksuz*, N. Gurler

ISTANBUL UNIVERSITY, ISTANBUL MEDICAL FACULTY, Istanbul, Turkey

Background: Vibrios have been recognized as human pathogens, and they can be acquired through either ingestion of contaminated seafood or contact of traumatized skin with seawater. *V.alginolyticus* occasionally causes life-threatening infections in immunocompromised individuals. We describe a case of sepsis due to *V. alginolyticus* isolated from catheter of 19-year-old patient with hypercholesterolemyType 2a while he was 7 years old.

The patient was admitted with high fever. He was applied routinally lipid aferesis. A catheter had inserted to him before one and a half years.

Methods: Blood cultures were sent from the catheter and peripheral vein of the patient to the laboratory and evaluated on the BACTEC 9120 system (Becton Dickinson, USA). The same day, a positive signal was taken from the cathether while blood culture obtained from the peripheral vein remained negative. The positive blood culture bottle was cultured on sheep-blood and chocolated agar. After 24 hours, straight or curved, Gram-negative, oxidase-positive colonies were seen on blood and chocolated agar. Yellow colonies were seen on thiosulfate-citrate-bile salts-sucrose (TCBS) agar after 24 hours of incubation. The identification was confirmed with another biochemical tests.

At the same time, the patient's general situation was deteriorated and went to sepsis. Blood cultures were sent again and the same bacteria was isolated again.

Results: The result of blood cultures was reported as *V.alginolyticus*. The bacteria were identified as *V. alginolyticus* by the API system (bioMerieux, France) at a 95.3% confidence level and by the VITEK 2 system (bioMerieux, France) at a 93% confidence level. The strain was only found to be resistant to ampicillin, but susceptible to the other antibiotic classes. The patient therapy improved by early diagnosis and appropriate and discharged. An identifiable source for this infection could not be found.

Conclusion: In conclusion, rapid and correct identification of the bacteria and early administration of appropriate antibiotics is essential for controlling invasive *Vibrio* infections, such as *V.alginolyticus* sepsis, especially in immunocompromised hosts. To the best of our knowledge, this is the first reported case of *V.alginolyticus* bacteremia reported in Turkey.

http://dx.doi.org/10.1016/j.ijid.2012.05.851